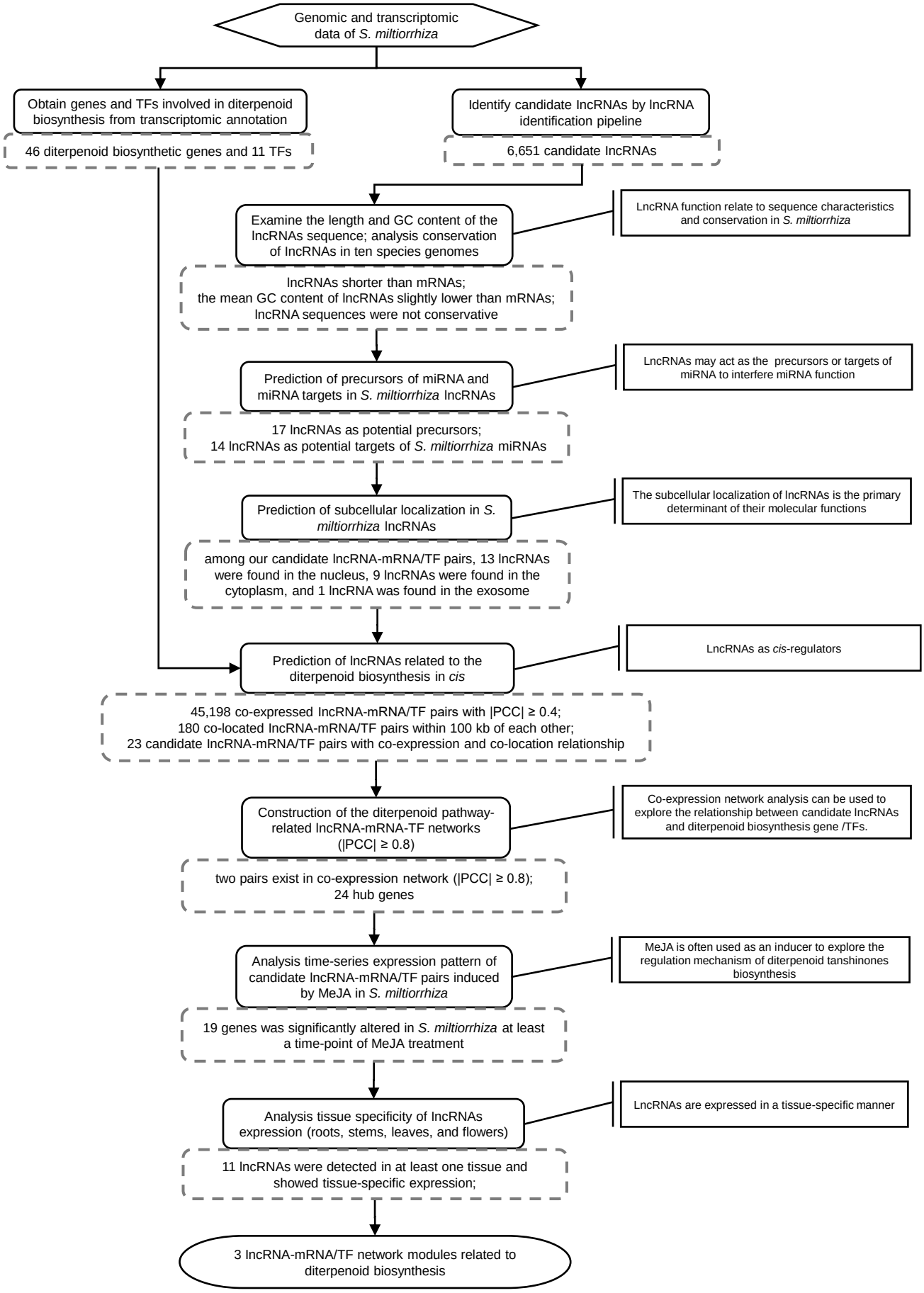
Genomic and transcriptomic data of S. miltiorrhiza
Obtain genes and TFs involved in diterpenoid biosynthesis from transcriptomic annotation
46 diterpenoid biosynthetic genes and 11 TFs
Identify candidate lncRNAs by lncRNA identification pipeline
6,651 candidate lncRNAs
Examine the length and GC content of the lncRNAs sequence; analysis conservation of lncRNAs in ten species genomes
LncRNA function relate to sequence characteristics and conservation in S. miltiorrhiza
lncRNAs shorter than mRNAs; the mean GC content of lncRNAs slightly lower than mRNAs; lncRNA sequences were not conservative
Prediction of precursors of miRNA and miRNA targets in S. miltiorrhiza lncRNAs
LncRNAs may act as the precursors or targets of miRNA to interfere miRNA function
17 lncRNAs as potential precursors; 14 lncRNAs as potential targets of S. miltiorrhiza miRNAs
Prediction of subcellular localization in S. miltiorrhiza lncRNAs
The subcellular localization of lncRNAs is the primary determinant of their molecular functions
among our candidate lncRNA-mRNA/TF pairs, 13 lncRNAs were found in the nucleus, 9 lncRNAs were found in the cytoplasm, and 1 lncRNA was found in the exosome
Prediction of lncRNAs related to the diterpenoid biosynthesis in cis
LncRNAs as cis-regulators
45,198 co-expressed lncRNA-mRNA/TF pairs with |PCC| ≥ 0.4; 180 co-located lncRNA-mRNA/TF pairs within 100 kb of each other; 23 candidate lncRNA-mRNA/TF pairs with co-expression and co-location relationship
Construction of the diterpenoid pathway-related lncRNA-mRNA-TF networks (|PCC| ≥ 0.8)
Co-expression network analysis can be used to explore the relationship between candidate lncRNAs and diterpenoid biosynthesis gene /TFs.
two pairs exist in co-expression network (|PCC| ≥ 0.8); 24 hub genes
Analysis time-series expression pattern of candidate lncRNA-mRNA/TF pairs induced by MeJA in S. miltiorrhiza
MeJA is often used as an inducer to explore the regulation mechanism of diterpenoid tanshinones biosynthesis
19 genes was significantly altered in S. miltiorrhiza at least a time-point of MeJA treatment
Analysis tissue specificity of lncRNAs expression (roots, stems, leaves, and flowers)
LncRNAs are expressed in a tissue-specific manner
11 lncRNAs were detected in at least one tissue and showed tissue-specific expression;
3 lncRNA-mRNA/TF network modules related to diterpenoid biosynthesis